

## SEQUENCE LISTING

<110> Acton, Susan L. et al.

<120> ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC  
DIAGNOSTIC USES THEREFOR

<130> MNI-132CP3

<140>

<141>

<150> 09/407,427

<151> 1999-09-29

<150> 09/163,648

<151> 1998-09-30

<150> 08/989,299

<151> 1997-12-11

<160> 107

<170> PatentIn Ver. 2.0

<210> 1

<211> 3396

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<213> Homo sapiens

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006080 "055E960

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&lt;211&gt; 805

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu  
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Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg  
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Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu  
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Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu  
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Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu  
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His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile  
245 250 255

Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly  
260 265 270

Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys  
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Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala  
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Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro  
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Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly  
340 345 350

Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp  
355 360 365

Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
370 375 380

Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
385 390 395 400

His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
405 410 415

His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn  
420 425 430

Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
435 440 445

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Variable	Mean	SD	Min	Max
Age	38.5	12.5	18	65
Gender	0.5	0.5	0	1
Marital Status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	3500	1500	1000	8000
Health Status	0.5	0.5	0	1
Exercise Frequency	2.5	1.5	0	5
Stress Level	4.5	1.5	1	7
Sleep Quality	3.5	1.5	1	7
Dietary Habits	0.5	0.5	0	1
Alcohol Consumption	0.5	0.5	0	1
Smoking Status	0.5	0.5	0	1
Family Size	2.5	1.5	1	5
Work Hours	40	10	20	60
Commuting Time	30	15	10	60
Job Satisfaction	4.5	1.5	1	7
Life Satisfaction	5.5	1.5	1	7
Overall Well-being	6.5	1.5	1	7

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile  
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Val Gln Thr Ser Phe  
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<212> DNA

<213> Homo sapiens

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&lt;210&gt; 4

&lt;211&gt; 732

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

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Gln Gln Val Thr Val Thr His Gly Thr Ser Ser Gln Ala Thr Thr Ser  
 35 40 45

Ser Gln Thr Thr Thr His Gln Ala Thr Ala His Gln Thr Ser Ala Gln  
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Ser Pro Asn Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu  
 65 70 75 80

Glu Tyr Asp Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu Ala  
 85 90 95

0063501.080900

Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu  
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 Gln Ala Arg Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile Lys  
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 Arg Ile Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala  
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 Gln Glu Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr  
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 Tyr Ser Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu  
 180 185 190  
 Glu Pro Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp  
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 Leu Lys Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp  
 340 345 350  
 Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn  
 355 360 365  
 Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His  
 370 375 380  
 Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln  
 385 390 395 400  
 Cys Thr Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met  
 405 410 415

006080" 030900

[illegible]

<210> 5  
<211> 732  
<212> PRT  
<213> Murine sp.

<220>  
<223> Description of Artificial Sequence: motifs

<400> 5  
Met Gly Gln Gly Trp Ala Thr Pro Gly Leu Pro Ser Phe Leu Phe Leu  
1 5 10 15  
Leu Leu Cys Cys Gly His His Leu Leu Val Leu Ser Gln Val Ala Thr  
20 25 30  
Asp His Val Thr Ala Asn Gln Gly Ile Thr Asn Gln Ala Thr Thr Arg  
35 40 45  
Ser Gln Thr Thr Thr His Gln Ala Thr Ile Asp Gln Thr Thr Gln Ile  
50 55 60  
Pro Asn Leu Glu Thr Asp Glu Ala Lys Ala Asp Arg Phe Val Glu Glu  
65 70 75 80  
Tyr Asp Arg Thr Ala Gln Val Leu Leu Asn Glu Tyr Ala Glu Ala Asn  
85 90 95  
Trp Gln Tyr Asn Thr Asn Ile Thr Ile Glu Gly Ser Lys Ile Leu Leu  
100 105 110  
Glu Lys Ser Thr Glu Val Ser Asn His Thr Leu Lys Tyr Gly Thr Arg  
115 120 125  
Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn Ser Ser Ile Lys Arg  
130 135 140  
Ile Ile Lys Lys Leu Gln Asn Leu Asp Arg Ala Val Leu Pro Pro Lys  
145 150 155 160  
Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met Glu Thr Thr Tyr  
165 170 175  
Ser Leu Ser Asn Ile Cys Tyr Thr Asn Gly Thr Cys Met Pro Leu Glu  
180 185 190  
Pro Asp Leu Thr Asn Met Met Ala Thr Ser Arg Lys Tyr Glu Glu Leu  
195 200 205  
Leu Trp Ala Trp Lys Ser Trp Arg Asp Lys Val Gly Arg Ala Ile Leu  
210 215 220  
Pro Phe Phe Pro Lys Tyr Val Glu Phe Ser Asn Lys Ile Ala Lys Leu  
225 230 235 240  
Asn Gly Tyr Thr Asp Ala Gly Asp Ser Trp Arg Ser Leu Tyr Glu Ser  
245 250 255  
Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln Glu Leu Gln Pro  
260 265 270

006080-10556950

[illegible]

595 600 605

Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Met Asn  
610 615 620

Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu Asn Arg Arg His  
625 630 635 640

Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala Pro Asn Thr Ala  
645 650 655

Arg Ala Glu Gly Ser Thr Ala Glu Ser Asn Arg Val Asn Phe Leu Gly  
660 665 670

Leu Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly Gln Trp Val Leu Leu  
675 680 685

Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val Gly Leu Ala His Arg  
690 695 700

Leu Tyr Asn Ile Arg Asn His His Ser Leu Arg Arg Pro His Arg Gly  
705 710 715 720

Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser  
725 730

&lt;210&gt; 6

&lt;211&gt; 737

&lt;212&gt; PRT

<213> *Cryptolagus cuniculus*

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: motifs

&lt;400&gt; 6

Met Gly Gln Gly Trp Ala Ala Pro Gly Leu Pro Ser Leu Leu Leu Leu  
1 5 10 15

Leu Leu Cys Cys Gly His Ser Leu Leu Val Pro Ser Arg Val Ala Ala  
20 25 30

Arg Arg Val Thr Val Asn Gln Gly Thr Thr Ser Gln Ala Thr Thr Thr  
35 40 45

Ser Lys Ala Thr Thr Ser Ile Arg Ala Thr Thr His Gln Thr Thr Ala  
50 55 60

His Gln Thr Thr Gln Ser Pro Asn Leu Val Thr Asp Glu Ala Glu Ala  
65 70 75 80

Ser Arg Phe Val Glu Glu Tyr Asp Arg Ser Phe Gln Ala Val Trp Asn  
85 90 95

Glu Tyr Ala Glu Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu  
100 105 110

Ala Ser Lys Ile Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr  
115 120 125

006080" 1055360

Leu Thr Tyr Gly Asn Trp Ala Arg Arg Phe Asp Val Ser Asn Phe Gln  
 130 135 140  
 Asn Ala Thr Ser Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Gln Arg  
 145 150 155 160  
 Ala Val Leu Pro Val Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu  
 165 170 175  
 Asp Met Glu Thr Ile Tyr Ser Val Ala Asn Val Cys Arg Val Asp Gly  
 180 185 190  
 Ser Cys Leu Gln Leu Glu Pro Asp Leu Thr Asn Leu Met Ala Thr Ser  
 195 200 205  
 Arg Lys Tyr Asp Glu Leu Leu Trp Val Trp Thr Ser Trp Arg Asp Lys  
 210 215 220  
 Val Gly Arg Ala Ile Leu Pro Tyr Phe Pro Lys Tyr Val Glu Phe Thr  
 225 230 235 240  
 Asn Lys Ala Ala Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp  
 245 250 255  
 Arg Ser Met Tyr Glu Thr Pro Thr Leu Glu Gln Asp Leu Glu Arg Leu  
 260 265 270  
 Phe Gln Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Gly  
 275 280 285  
 Arg Ala Leu His Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly  
 290 295 300  
 Pro Ile Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser  
 305 310 315 320  
 Asn Ile Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Ser Thr Met Asp  
 325 330 335  
 Ala Thr Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Met Phe  
 340 345 350  
 Glu Glu Ala Asp Lys Phe Phe Ile Ser Leu Gly Leu Leu Pro Val Pro  
 355 360 365  
 Pro Glu Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg  
 370 375 380  
 Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp  
 385 390 395 400  
 Phe Arg Ile Lys Gln Cys Thr Thr Val Asn Met Glu Asp Leu Val Val  
 405 410 415  
 Val His His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp  
 420 425 430  
 Leu Pro Val Ala Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala  
 435 440 445

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Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His  
450 455 460

Ser Ile Asn Leu Leu Ser Ser Glu Gly Gly Gly Tyr Glu His Asp Ile  
465 470 475 480

Asn Phe Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe  
485 490 495

Ser Tyr Leu Val Asp Glu Trp Arg Trp Arg Val Phe Asp Gly Ser Ile  
500 505 510

Thr Lys Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr  
515 520 525

Gln Gly Leu Cys Pro Pro Ala Pro Arg Ser Gln Gly Asp Phe Asp Pro  
530 535 540

Gly Ala Lys Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe  
545 550 555 560

Val Ser Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Lys Ala  
565 570 575

Ala Gly His Thr Gly Pro Leu His Thr Cys Asp Ile Tyr Gln Ser Lys  
580 585 590

Glu Ala Gly Lys Arg Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys  
595 600 605

Pro Trp Pro Glu Ala Met Lys Val Ile Thr Gly Gln Pro Asn Met Ser  
610 615 620

Ala Ser Ala Met Met Asn Tyr Phe Lys Pro Leu Met Asp Trp Leu Leu  
625 630 635 640

Thr Glu Asn Gly Arg His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Thr  
645 650 655

Trp Thr Pro Asn Ser Ala Arg Ser Glu Gly Ser Leu Pro Asp Ser Gly  
660 665 670

Arg Val Asn Phe Leu Gly Met Asn Leu Asp Ala Gln Gln Ala Arg Val  
675 680 685

Gly Gln Trp Val Leu Leu Phe Leu Gly Val Ala Leu Leu Leu Ala Ser  
690 695 700

Leu Gly Leu Thr Gln Arg Leu Phe Ser Ile Arg Tyr Gln Ser Leu Arg  
705 710 715 720

Gln Pro His His Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His  
725 730 735

Ser

&lt;210&gt; 7

&lt;211&gt; 1306

&lt;212&gt; PRT

0063501 080900



&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: motifs

&lt;400&gt; 7

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Met Gly Ala Ala Ser Gly Arg Arg Gly Pro Gly Leu Leu Leu Pro Leu
 1           5           10           15

Pro Leu Leu Leu Leu Leu Pro Pro Gln Pro Ala Leu Ala Leu Asp Pro
          20           25           30

Gly Leu Gln Pro Gly Asn Phe Ser Ala Asp Glu Ala Gly Ala Gln Leu
          35           40           45

Phe Ala Gln Ser Tyr Asn Ser Ser Ala Glu Gln Val Leu Phe Gln Ser
          50           55           60

Val Ala Ala Ser Trp Ala His Asp Thr Asn Ile Thr Ala Glu Asn Ala
          65           70           75           80

Arg Arg Gln Glu Glu Ala Ala Leu Leu Ser Gln Glu Phe Ala Glu Ala
          85           90           95

Trp Gly Gln Lys Ala Lys Glu Leu Tyr Glu Pro Ile Trp Gln Asn Phe
          100          105          110

Thr Asp Pro Gln Leu Arg Arg Ile Ile Gly Ala Val Arg Thr Leu Gly
          115          120          125

Ser Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln Tyr Asn Ala Leu Leu
          130          135          140

Ser Asn Met Ser Arg Ile Tyr Ser Thr Ala Lys Val Cys Leu Pro Asn
          145          150          155          160

Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Asp Leu Thr Asn Ile Leu
          165          170          175

Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe Ala Trp Glu Gly Trp
          180          185          190

His Asn Ala Ala Gly Ile Pro Leu Lys Pro Leu Tyr Glu Asp Phe Thr
          195          200          205

Ala Leu Ser Asn Glu Ala Tyr Lys Gln Asp Gly Phe Thr Asp Thr Gly
          210          215          220

Ala Tyr Trp Arg Ser Trp Tyr Asn Ser Pro Thr Phe Glu Asp Asp Leu
          225          230          235          240

Glu His Leu Tyr Gln Gln Leu Glu Pro Leu Tyr Leu Asn Leu His Ala
          245          250          255

Phe Val Arg Arg Ala Leu His Arg Arg Tyr Gly Asp Arg Tyr Ile Asn
          260          265          270

Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly Asp Met Trp Ala Gln
          275          280          285

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Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro Phe Pro Asp Lys Pro  
290 295 300

Asn Leu Asp Val Thr Ser Thr Met Leu Gln Gln Gly Trp Asn Ala Thr  
305 310 315 320

His Met Phe Arg Val Ala Glu Glu Phe Phe Thr Ser Leu Glu Leu Ser  
325 330 335

Pro Met Pro Pro Glu Phe Trp Glu Gly Ser Met Leu Glu Lys Pro Ala  
340 345 350

Asp Gly Arg Glu Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn  
355 360 365

Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg Val Thr Met Asp Gln  
370 375 380

Leu Ser Thr Val His His Glu Met Gly His Ile Gln Tyr Tyr Leu Gln  
385 390 395 400

Tyr Lys Asp Leu Pro Val Ser Leu Arg Arg Gly Ala Asn Pro Gly Phe  
405 410 415

His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Glu  
420 425 430

His Leu His Lys Ile Gly Leu Leu Asp Arg Val Thr Asn Asp Thr Glu  
435 440 445

Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu Lys Ile Ala Phe  
450 455 460

Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp Gly Val Phe Ser  
465 470 475 480

Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp Trp Trp Tyr Leu Arg  
485 490 495

Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Thr Arg Asn Glu Thr His  
500 505 510

Phe Asp Ala Gly Ala Lys Phe His Val Pro Asn Val Thr Pro Tyr Ile  
515 520 525

Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe His Glu Ala Leu  
530 535 540

Cys Lys Glu Ala Gly Tyr Glu Gly Pro Leu His Gln Cys Asp Ile Tyr  
545 550 555 560

Arg Ser Thr Lys Ala Gly Ala Lys Leu Arg Lys Val Leu Gln Ala Gly  
565 570 575

Ser Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met Val Gly Leu Asp  
580 585 590

Ala Leu Asp Ala Gln Pro Leu Leu Lys Tyr Phe Gln Pro Val Thr Gln  
595 600 605

0063501-00000

Trp Leu Gln Glu Gln Asn Gln Gln Asn Gly Glu Val Leu Gly Trp Pro  
610 615 620

Glu Tyr Gln Trp His Pro Pro Leu Pro Asp Asn Tyr Pro Glu Gly Ile  
625 630 635 640

Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu Glu Tyr  
645 650 655

Asp Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu Ala Asn Trp  
660 665 670

Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu Leu Gln  
675 680 685

Lys Asn Met Gln Ile Ala Asn His Thr Leu Lys Tyr Gly Thr Gln Ala  
690 695 700

Arg Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile Lys Arg Ile  
705 710 715 720

Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala Gln Glu  
725 730 735

Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr Tyr Ser  
740 745 750

Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu Glu Pro  
755 760 765

Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp Leu Leu  
770 775 780

Trp Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala Ile Leu Gln  
785 790 795 800

Phe Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala Arg Leu Asn  
805 810 815

Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr Glu Thr Pro  
820 825 830

Ser Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu Gln Pro Leu  
835 840 845

Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg His Tyr  
850 855 860

Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala His Leu Leu  
865 870 875 880

Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu Val Val  
885 890 895

Pro Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala Met Leu Lys  
900 905 910

Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp Phe Phe  
915 920 925

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Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys Ser  
930 935 940

Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser  
945 950 955 960

Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys Thr  
965 970 975

Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met Gly His  
980 985 990

Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu Arg Glu  
995 1000 1005

Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu  
1010 1015 1020

Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu Ser Ser  
1025 1030 1035 1040

Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met Lys Met Ala  
1045 1050 1055

Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val Asp Gln Trp  
1060 1065 1070

Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn Gln  
1075 1080 1085

Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro Val  
1090 1095 1100

Pro Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe His Ile Pro  
1105 1110 1115 1120

Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile Ile Gln Phe  
1125 1130 1135

Gln Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr Gly Pro Leu  
1140 1145 1150

His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln Arg Leu Ala  
1155 1160 1165

Thr Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu Ala Met Gln  
1170 1175 1180

Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Leu Ser Tyr  
1185 1190 1195 1200

Phe Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu Leu His Gly  
1205 1210 1215

Glu Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn Ser Ala Arg  
1220 1225 1230

Ser Glu Gly Pro Leu Pro Asp Ser Gly Arg Val Ser Phe Leu Gly Leu  
1235 1240 1245

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Asp Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp Leu Leu Leu Phe  
 1250 1255 1260

Leu Gly Ile Ala Leu Leu Val Ala Thr Leu Gly Leu Ser Gln Arg Leu  
 1265 1270 1275 1280

Phe Ser Ile Arg His Arg Ser Leu His Arg His Ser His Gly Pro Gln  
 1285 1290 1295

Phe Gly Ser Glu Val Glu Leu Arg His Ser  
 1300 1305

<210> 8

<211> 1312

<212> PRT

<213> Murine sp.

<220>

<223> Description of Artificial Sequence: motifs

<400> 8

Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro  
 1 5 10 15

Leu Leu Met Leu Ser Leu Leu Val Leu Leu Leu Gln Pro Ser Pro Ala  
 20 25 30

Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Pro Asp Glu  
 35 40 45

Ala Gly Ala Gln Leu Phe Ala Glu Ser Tyr Asn Ser Ser Ala Glu Val  
 50 55 60

Val Met Phe Gln Ser Thr Val Ala Ser Trp Ala His Asp Thr Asn Ile  
 65 70 75 80

Thr Glu Glu Asn Ala Arg Arg Gln Glu Glu Ala Ala Leu Val Ser Gln  
 85 90 95

Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu Ser  
 100 105 110

Ile Trp Gln Asn Phe Thr Asp Ser Lys Leu Arg Arg Ile Ile Gly Ser  
 115 120 125

Ile Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Gln Arg Gln Gln  
 130 135 140

Tyr Asn Ser Leu Leu Ser Asn Met Ser Arg Ile Tyr Ser Thr Gly Lys  
 145 150 155 160

Val Cys Phe Pro Asn Lys Thr Ala Thr Cys Trp Ser Leu Asp Pro Glu  
 165 170 175

Leu Thr Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Lys Leu Leu Phe  
 180 185 190

Ala Trp Glu Gly Trp His Asp Ala Val Gly Ile Pro Leu Lys Pro Leu  
 195 200 205

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Tyr Gln Asp Phe Thr Ala Ile Ser Asn Glu Ala Tyr Arg Gln Asp Asp  
210 215 220

Phe Ser Asp Thr Gly Ala Phe Trp Arg Ser Trp Tyr Glu Ser Pro Ser  
225 230 235 240

Phe Glu Glu Ser Leu Glu His Ile Tyr His Gln Leu Glu Pro Leu Tyr  
245 250 255

Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg Arg Tyr Gly  
260 265 270

Asp Lys Tyr Val Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly  
275 280 285

Asp Met Trp Ala Gln Ser Trp Glu Asn Ile Tyr Asp Met Val Val Pro  
290 295 300

Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys  
305 310 315 320

Gly Trp Asn Ala Thr His Met Phe Arg Val Ser Glu Glu Phe Phe Thr  
325 330 335

Ser Leu Gly Leu Ser Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met  
340 345 350

Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser Ala  
355 360 365

Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Arg  
370 375 380

Val Thr Met Glu Gln Leu Ala Thr Val His His Glu Met Gly His Val  
385 390 395 400

Gln Tyr Tyr Leu Gln Tyr Lys Asp Leu His Val Ser Leu Arg Arg Gly  
405 410 415

Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser  
420 425 430

Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val  
435 440 445

Thr Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu  
450 455 460

Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg  
465 470 475 480

Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Phe Asp  
485 490 495

Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Ala  
500 505 510

Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro Asn  
515 520 525

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Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln  
530 535 540

Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu His  
545 550 555 560

Gln Cys Asp Ile Tyr Gln Ser Thr Gln Ala Gly Ala Lys Leu Lys Gln  
565 570 575

Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp  
580 585 590

Leu Val Gly Ser Asp Ala Leu Asp Ala Lys Ala Leu Leu Glu Tyr Phe  
595 600 605

Gln Pro Val Ser Gln Trp Leu Glu Glu Gln Asn Gln Arg Asn Gly Glu  
610 615 620

Val Leu Gly Trp Pro Glu Asn Gln Trp Arg Pro Pro Leu Pro Asp Asn  
625 630 635 640

Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asp Arg  
645 650 655

Phe Val Glu Glu Tyr Asp Arg Thr Ala Gln Val Leu Leu Asn Glu Tyr  
660 665 670

Ala Glu Ala Asn Trp Gln Tyr Asn Thr Asn Ile Thr Ile Glu Gly Ser  
675 680 685

Lys Ile Leu Leu Glu Lys Ser Thr Glu Val Ser Asn His Thr Leu Lys  
690 695 700

Tyr Gly Thr Arg Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn Ser  
705 710 715 720

Ser Ile Lys Arg Ile Ile Lys Lys Leu Gln Asn Leu Asp Arg Ala Val  
725 730 735

Leu Pro Pro Lys Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp Met  
740 745 750

Glu Thr Thr Tyr Ser Leu Ser Asn Ile Cys Tyr Thr Asn Gly Thr Cys  
755 760 765

Met Pro Leu Glu Pro Asp Leu Thr Asn Met Met Ala Thr Ser Arg Lys  
770 775 780

Tyr Glu Glu Leu Leu Trp Ala Trp Lys Ser Trp Arg Asp Lys Val Gly  
785 790 795 800

Arg Ala Ile Leu Pro Phe Phe Pro Lys Tyr Val Glu Phe Ser Asn Lys  
805 810 815

Ile Ala Lys Leu Asn Gly Tyr Thr Asp Ala Gly Asp Ser Trp Arg Ser  
820 825 830

Leu Tyr Glu Ser Asp Asn Leu Glu Gln Asp Leu Glu Lys Leu Tyr Gln  
835 840 845

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Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ser  
850 855 860

Leu His Arg His Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro Ile  
865 870 875 880

Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile  
885 890 895

Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Pro Asn Ile Asp Ala Thr  
900 905 910

Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys Glu  
915 920 925

Ala Asp Asn Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu  
930 935 940

Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val  
945 950 955 960

Val Cys His Pro Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg  
965 970 975

Ile Lys Gln Cys Thr Ser Val Asn Met Glu Asp Leu Val Ile Ala His  
980 985 990

His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro  
995 1000 1005

Val Thr Phe Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly  
1010 1015 1020

Asp Ile Met Ala Leu Ser Val Ser Thr Pro Lys His Leu Tyr Ser Leu  
1025 1030 1035 1040

Asn Leu Leu Ser Thr Glu Gly Ser Gly Tyr Glu Tyr Asp Ile Asn Phe  
1045 1050 1055

Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr  
1060 1065 1070

Leu Ile Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys  
1075 1080 1085

Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly  
1090 1095 1100

Leu Cys Pro Pro Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ser  
1105 1110 1115 1120

Lys Phe His Val Pro Ala Asn Val Pro Tyr Val Arg Tyr Phe Val Ser  
1125 1130 1135

Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala Gly  
1140 1145 1150

His Thr Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala  
1155 1160 1165

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Gly Lys Leu Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp  
 1170 1175 1180

Pro Glu Ala Met Lys Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser  
 1185 1190 1195 1200

Ala Met Met Asn Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr Glu  
 1205 1210 1215

Asn Arg Arg His Gly Glu Thr Leu Gly Trp Pro Glu Tyr Asn Trp Ala  
 1220 1225 1230

Pro Asn Thr Ala Arg Ala Glu Gly Ser Thr Ala Glu Ser Asn Arg Val  
 1235 1240 1245

Asn Phe Leu Gly Leu Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly Gln  
 1250 1255 1260

Trp Val Leu Leu Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val Gly  
 1265 1270 1275 1280

Leu Ala His Arg Leu Tyr Asn Ile Arg Asn His His Ser Leu Arg Arg  
 1285 1290 1295

Pro His Arg Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser  
 1300 1305 1310

<210> 9

<211> 1313

<212> PRT

<213> Rattus rattus

<220>

<223> Description of Artificial Sequence: motifs

<400> 9

Met Gly Ala Ala Ser Gly Gln Arg Gly Arg Trp Pro Leu Ser Pro Pro  
 1 5 10 15

Leu Leu Met Leu Ser Leu Leu Leu Leu Leu Leu Leu Pro Pro Ser Pro  
 20 25 30

Ala Pro Ala Leu Asp Pro Gly Leu Gln Pro Gly Asn Phe Ser Ala Asp  
 35 40 45

Glu Ala Gly Ala Gln Leu Phe Ala Asp Ser Tyr Asn Ser Ser Ala Glu  
 50 55 60

Val Val Met Phe Gln Ser Thr Ala Ala Ser Trp Ala His Asp Thr Asn  
 65 70 75 80

Ile Thr Glu Glu Asn Ala Arg Leu Gln Glu Glu Ala Ala Leu Ile Asn  
 85 90 95

Gln Glu Phe Ala Glu Val Trp Gly Lys Lys Ala Lys Glu Leu Tyr Glu  
 100 105 110

006080" T055E950

Parameter	Control		100 mg/kg		200 mg/kg		400 mg/kg		800 mg/kg	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD	Mean	SD
1. Body weight (g)	200.0	10.0	200.0	10.0	200.0	10.0	200.0	10.0	200.0	10.0
2. Food intake (g)	10.0	2.0	10.0	2.0	10.0	2.0	10.0	2.0	10.0	2.0
3. Water intake (ml)	5.0	1.0	5.0	1.0	5.0	1.0	5.0	1.0	5.0	1.0
4. Urine output (ml)	1.0	0.5	1.0	0.5	1.0	0.5	1.0	0.5	1.0	0.5
5. Fecal output (g)	1.0	0.5	1.0	0.5	1.0	0.5	1.0	0.5	1.0	0.5
6. Hemoglobin (g/dl)	15.0	1.0	15.0	1.0	15.0	1.0	15.0	1.0	15.0	1.0
7. Hematocrit (%)	45.0	2.0	45.0	2.0	45.0	2.0	45.0	2.0	45.0	2.0
8. RBC count (10 <sup>12</sup> /L)	5.0	0.5	5.0	0.5	5.0	0.5	5.0	0.5	5.0	0.5
9. WBC count (10 <sup>9</sup> /L)	10.0	2.0	10.0	2.0	10.0	2.0	10.0	2.0	10.0	2.0
10. Platelet count (10 <sup>9</sup> /L)	150.0	20.0	150.0	20.0	150.0	20.0	150.0	20.0	150.0	20.0
11. Prothrombin time (s)	12.0	1.0	12.0	1.0	12.0	1.0	12.0	1.0	12.0	1.0
12. Activated partial thromboplastin time (s)	30.0	2.0	30.0	2.0	30.0	2.0	30.0	2.0	30.0	2.0
13. Fibrinogen (g/dl)	0.5	0.1	0.5	0.1	0.5	0.1	0.5	0.1	0.5	0.1
14. Creatinine (mg/dl)	0.2	0.05	0.2	0.05	0.2	0.05	0.2	0.05	0.2	0.05
15. BUN (mg/dl)	10.0	2.0	10.0	2.0	10.0	2.0	10.0	2.0	10.0	2.0
16. ALT (U/L)	20.0	5.0	20.0	5.0	20.0	5.0	20.0	5.0	20.0	5.0
17. AST (U/L)	30.0	10.0	30.0	10.0	30.0	10.0	30.0	10.0	30.0	10.0
18. ALP (U/L)	100.0	20.0	100.0	20.0	100.0	20.0	100.0	20.0	100.0	20.0
19. Bilirubin (mg/dl)	0.1	0.02	0.1	0.02	0.1	0.02	0.1	0.02	0.1	0.02
20. Urinary protein (mg/day)	10.0	5.0	10.0	5.0	10.0	5.0	10.0	5.0	10.0	5.0
21. Urinary creatinine (mg/day)	1.0	0.5	1.0	0.5	1.0	0.5	1.0	0.5	1.0	0.5
22. Urinary albumin (mg/day)	0.1	0.05	0.1	0.05	0.1	0.05	0.1	0.05	0.1	0.05
23. Urinary glucose (mg/day)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
24. Urinary ketones (mg/day)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
25. Urinary pH	7.0	0.5	7.0	0.5	7.0	0.5	7.0	0.5	7.0	0.5
26. Urinary specific gravity	1.020	0.010	1.020	0.010	1.020	0.010	1.020	0.010	1.020	0.010
27. Urinary osmolality (mOsm/kg)	300	20	300	20	300	20	300	20	300	20
28. Urinary sodium (mEq/day)	100	20	100	20	100	20	100	20	100	20
29. Urinary potassium (mEq/day)	50	10	50	10	50	10	50	10	50	10
30. Urinary calcium (mEq/day)	20	5	20	5	20	5	20	5	20	5
31. Urinary magnesium (mEq/day)	10	2	10	2	10	2	10	2	10	2
32. Urinary chloride (mEq/day)	100	20	100	20	100	20	100	20	100	20
33. Urinary phosphate (mEq/day)	20	5	20	5	20	5	20	5	20	5
34. Urinary sulfate (mEq/day)	10	2	10	2	10	2	10	2	10	2
35. Urinary nitrate (mEq/day)	0	0	0							

Ser Val Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp Arg  
435 440 445

Val Ala Asn Asp Ile Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala  
450 455 460

Leu Glu Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp  
465 470 475 480

Arg Trp Gly Val Phe Ser Gly Arg Thr Pro Pro Ser Arg Tyr Asn Tyr  
485 490 495

Asp Trp Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val  
500 505 510

Ala Arg Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro  
515 520 525

Ser Val Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe  
530 535 540

Gln Phe His Gln Ala Leu Cys Lys Glu Ala Gly His Gln Gly Pro Leu  
545 550 555 560

His Gln Cys Asp Ile Tyr Gln Ser Thr Lys Ala Gly Ala Lys Leu Gln  
565 570 575

Gln Val Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys  
580 585 590

Asp Leu Val Gly Ser Asp Ala Leu Asp Ala Ser Ala Leu Met Glu Tyr  
595 600 605

Phe Gln Pro Val Ser Gln Trp Leu Gln Glu Gln Asn Gln Arg Asn Gly  
610 615 620

Glu Val Leu Gly Trp Pro Glu Tyr Gln Trp Arg Pro Pro Leu Pro Asp  
625 630 635 640

Asn Tyr Pro Glu Gly Ile Asp Leu Glu Thr Asp Glu Ala Lys Ala Asn  
645 650 655

Arg Phe Val Glu Glu Tyr Asp Arg Thr Ala Lys Val Leu Trp Asn Glu  
660 665 670

Tyr Ala Glu Ala Asn Trp His Tyr Asn Thr Asn Ile Thr Ile Glu Gly  
675 680 685

Ser Lys Ile Leu Leu Gln Lys Asn Lys Glu Val Ser Asn His Thr Leu  
690 695 700

Lys Tyr Gly Thr Trp Ala Lys Thr Phe Asp Val Ser Asn Phe Gln Asn  
705 710 715 720

Ser Thr Ile Lys Arg Ile Ile Lys Lys Val Gln Asn Val Asp Arg Ala  
725 730 735

Val Leu Pro Pro Asn Glu Leu Glu Glu Tyr Asn Gln Ile Leu Leu Asp  
740 745 750

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Met Glu Thr Thr Tyr Ser Val Ala Asn Val Cys Tyr Thr Asn Gly Thr  
755 760 765

Cys Leu Ser Leu Glu Pro Asp Leu Thr Asn Ile Met Ala Thr Ser Arg  
770 775 780

Lys Tyr Glu Glu Leu Leu Trp Val Trp Lys Ser Trp Arg Asp Lys Val  
785 790 795 800

Gly Arg Ala Ile Leu Pro Phe Phe Pro Lys Tyr Val Asp Phe Ser Asn  
805 810 815

Lys Ile Ala Lys Leu Asn Gly Tyr Ser Asp Ala Gly Asp Ser Trp Arg  
820 825 830

Ser Ser Tyr Glu Ser Asp Asp Leu Glu Gln Asp Leu Glu Lys Leu Tyr  
835 840 845

Gln Glu Leu Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg  
850 855 860

Ser Leu His Arg His Tyr Gly Ser Glu Tyr Ile Asn Leu Asp Gly Pro  
865 870 875 880

Ile Pro Ala His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn  
885 890 895

Ile Tyr Asp Leu Val Ala Pro Phe Pro Ser Ala Pro Ser Ile Asp Ala  
900 905 910

Thr Glu Ala Met Ile Lys Gln Gly Trp Thr Pro Arg Arg Ile Phe Lys  
915 920 925

Glu Ala Asp Asn Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro  
930 935 940

Glu Phe Trp Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu  
945 950 955 960

Val Val Cys His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe  
965 970 975

Arg Ile Lys Gln Cys Thr Ser Val Asn Met Glu Glu Leu Val Ile Ala  
980 985 990

His His Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu  
995 1000 1005

Pro Val Thr Phe Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile  
1010 1015 1020

Gly Asp Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser  
1025 1030 1035 1040

Leu Asn Leu Leu Ser Glu Gly Ser Gly Tyr Glu His Asp Ile Asn  
1045 1050 1055

Phe Leu Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser  
1060 1065 1070

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Tyr Leu Ile Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr  
 1075 1080 1085

Lys Glu Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln  
 1090 1095 1100

Gly Leu Cys Pro Pro Val Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly  
 1105 1110 1115 1120

Ser Lys Phe His Val Pro Ala Asn Val Pro Tyr Ile Arg Tyr Phe Ile  
 1125 1130 1135

Ser Phe Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Arg Ala Ala  
 1140 1145 1150

Gly His Thr Gly Pro Leu Tyr Lys Cys Asp Ile Tyr Gln Ser Lys Glu  
 1155 1160 1165

Ala Gly Lys Leu Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Gln  
 1170 1175 1180

Trp Pro Glu Ala Met Lys Ile Ile Thr Gly Gln Pro Asn Met Ser Ala  
 1185 1190 1195 1200

Ser Ala Ile Met Asn Tyr Phe Lys Pro Leu Thr Glu Trp Leu Val Thr  
 1205 1210 1215

Glu Asn Arg Arg His Gly Glu Thr Leu Gly Trp Pro Glu Tyr Thr Trp  
 1220 1225 1230

Thr Pro Asn Thr Ala Arg Ala Glu Gly Ser Leu Pro Glu Ser Ser Arg  
 1235 1240 1245

Val Asn Phe Leu Gly Met Tyr Leu Glu Pro Gln Gln Ala Arg Val Gly  
 1250 1255 1260

Gln Trp Val Leu Leu Phe Leu Gly Val Ala Leu Leu Val Ala Thr Val  
 1265 1270 1275 1280

Gly Leu Ala His Arg Leu Tyr Asn Ile His Asn His His Ser Leu Arg  
 1285 1290 1295

Arg Pro His Arg Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His  
 1300 1305 1310

Ser

<210> 10

<211> 1310

<212> PRT

<213> *Oryctolagus cuniculus*

<220>

<223> Description of Artificial Sequence: motifs

<400> 10

Met Gly Ala Ala Pro Gly Arg Arg Gly Pro Arg Leu Leu Arg Pro Pro  
 1 5 10 15

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Pro Pro Leu Leu Leu Leu Leu Leu Leu Leu Arg Pro Pro Pro Ala Ala  
20 25 30

Leu Thr Leu Asp Pro Gly Leu Leu Pro Gly Asp Phe Ala Ala Asp Glu  
35 40 45

Ala Gly Ala Arg Leu Phe Ala Ser Ser Tyr Asn Ser Ser Ala Glu Gln  
50 55 60

Val Leu Phe Arg Ser Thr Ala Ala Ser Trp Ala His Asp Thr Asn Ile  
65 70 75 80

Thr Ala Glu Asn Ala Arg Arg Gln Glu Glu Glu Ala Leu Leu Ser Gln  
85 90 95

Glu Phe Ala Glu Ala Trp Gly Lys Lys Ala Lys Glu Leu Tyr Asp Pro  
100 105 110

Val Trp Gln Asn Phe Thr Asp Pro Glu Leu Arg Arg Ile Ile Gly Ala  
115 120 125

Val Arg Thr Leu Gly Pro Ala Asn Leu Pro Leu Ala Lys Arg Gln Gln  
130 135 140

Tyr Asn Ser Leu Leu Ser Asn Met Ser Gln Ile Tyr Ser Thr Gly Lys  
145 150 155 160

Val Cys Phe Pro Asn Lys Thr Ala Ser Cys Trp Ser Leu Asp Pro Asp  
165 170 175

Leu Asn Asn Ile Leu Ala Ser Ser Arg Ser Tyr Ala Met Leu Leu Phe  
180 185 190

Ala Trp Glu Gly Trp His Asn Ala Val Gly Ile Pro Leu Lys Pro Leu  
195 200 205

Tyr Gln Glu Phe Thr Ala Leu Ser Asn Glu Ala Tyr Arg Gln Asp Gly  
210 215 220

Phe Ser Asp Thr Gly Ala Tyr Trp Arg Ser Trp Tyr Asp Ser Pro Thr  
225 230 235 240

Phe Glu Glu Asp Leu Glu Arg Ile Tyr His Gln Leu Glu Pro Leu Tyr  
245 250 255

Leu Asn Leu His Ala Tyr Val Arg Arg Val Leu His Arg Arg Tyr Gly  
260 265 270

Asp Arg Tyr Ile Asn Leu Arg Gly Pro Ile Pro Ala His Leu Leu Gly  
275 280 285

Asn Met Trp Ala Gln Ser Trp Glu Ser Ile Tyr Asp Met Val Val Pro  
290 295 300

Phe Pro Asp Lys Pro Asn Leu Asp Val Thr Ser Thr Met Val Gln Lys  
305 310 315 320

Gly Trp Asn Ala Thr His Met Phe Arg Val Ala Glu Glu Phe Phe Thr  
325 330 335

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Ser Leu Gly Leu Leu Pro Met Pro Pro Glu Phe Trp Ala Glu Ser Met  
340 345 350

Leu Glu Lys Pro Glu Asp Gly Arg Glu Val Val Cys His Ala Ser Ala  
355 360 365

Trp Asp Phe Tyr Asn Arg Lys Asp Phe Arg Ile Lys Gln Cys Thr Gln  
370 375 380

Val Thr Met Asp Gln Leu Ser Thr Val His His Glu Met Gly His Val  
385 390 395 400

Gln Tyr Tyr Leu Gln Tyr Lys Asp Gln Pro Val Ser Leu Arg Arg Ala  
405 410 415

Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser Val  
420 425 430

Ser Thr Pro Ala His Leu His Lys Ile Gly Leu Leu Asp His Val Thr  
435 440 445

Asn Asp Thr Glu Ser Asp Ile Asn Tyr Leu Leu Lys Met Ala Leu Glu  
450 455 460

Lys Ile Ala Phe Leu Pro Phe Gly Tyr Leu Val Asp Gln Trp Arg Trp  
465 470 475 480

Gly Val Phe Ser Gly Arg Thr Pro Ser Ser Arg Tyr Asn Phe Asp Trp  
485 490 495

Trp Tyr Leu Arg Thr Lys Tyr Gln Gly Ile Cys Pro Pro Val Val Arg  
500 505 510

Asn Glu Thr His Phe Asp Ala Gly Ala Lys Phe His Ile Pro Ser Val  
515 520 525

Thr Pro Tyr Ile Arg Tyr Phe Val Ser Phe Val Leu Gln Phe Gln Phe  
530 535 540

His Gln Ala Leu Cys Met Glu Ala Gly His Gln Gly Pro Leu His Gln  
545 550 555 560

Cys Asp Ile Tyr Gln Ser Thr Arg Ala Gly Ala Lys Leu Arg Ala Val  
565 570 575

Leu Gln Ala Gly Cys Ser Arg Pro Trp Gln Glu Val Leu Lys Asp Met  
580 585 590

Val Ala Ser Asp Ala Leu Asp Ala Gln Pro Leu Leu Asp Tyr Phe Gln  
595 600 605

Pro Val Thr Gln Trp Leu Gln Glu Gln Asn Glu Arg Asn Gly Glu Val  
610 615 620

Leu Gly Trp Pro Glu Tyr Gln Trp Arg Pro Pro Leu Pro Asn Asn Tyr  
625 630 635 640

Pro Glu Gly Ile Asp Leu Val Thr Asp Glu Ala Glu Ala Ser Arg Phe  
645 650 655

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Val	Glu	Glu	Tyr	Asp	Arg	Ser	Phe	Gln	Ala	Val	Trp	Asn	Glu	Tyr	Ala
			660					665					670		
Glu	Ala	Asn	Trp	Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Thr	Glu	Ala	Ser	Lys
		675					680					685			
Ile	Leu	Leu	Gln	Lys	Asn	Met	Gln	Ile	Ala	Asn	His	Thr	Leu	Thr	Tyr
	690					695					700				
Gly	Asn	Trp	Ala	Arg	Arg	Phe	Asp	Val	Ser	Asn	Phe	Gln	Asn	Ala	Thr
705					710					715					720
Ser	Lys	Arg	Ile	Ile	Lys	Lys	Val	Gln	Asp	Leu	Gln	Arg	Ala	Val	Leu
				725					730					735	
Pro	Val	Lys	Glu	Leu	Glu	Glu	Tyr	Asn	Gln	Ile	Leu	Leu	Asp	Met	Glu
			740					745					750		
Thr	Ile	Tyr	Ser	Val	Ala	Asn	Val	Cys	Arg	Val	Asp	Gly	Ser	Cys	Leu
		755					760					765			
Gln	Leu	Glu	Pro	Asp	Leu	Thr	Asn	Leu	Met	Ala	Thr	Ser	Arg	Lys	Tyr
	770					775					780				
Asp	Glu	Leu	Leu	Trp	Val	Trp	Thr	Ser	Trp	Arg	Asp	Lys	Val	Gly	Arg
785					790					795					800
Ala	Ile	Leu	Pro	Tyr	Phe	Pro	Lys	Tyr	Val	Glu	Phe	Thr	Asn	Lys	Ala
				805					810					815	
Ala	Arg	Leu	Asn	Gly	Tyr	Val	Asp	Ala	Gly	Asp	Ser	Trp	Arg	Ser	Met
			820					825					830		
Tyr	Glu	Thr	Pro	Thr	Leu	Glu	Gln	Asp	Leu	Glu	Arg	Leu	Phe	Gln	Glu
		835					840					845			
Leu	Gln	Pro	Leu	Tyr	Leu	Asn	Leu	His	Ala	Tyr	Val	Gly	Arg	Ala	Leu
	850					855					860				
His	Arg	His	Tyr	Gly	Ala	Gln	His	Ile	Asn	Leu	Glu	Gly	Pro	Ile	Pro
865					870					875					880
Ala	His	Leu	Leu	Gly	Asn	Met	Trp	Ala	Gln	Thr	Trp	Ser	Asn	Ile	Tyr
				885					890					895	
Asp	Leu	Val	Ala	Pro	Phe	Pro	Ser	Ala	Ser	Thr	Met	Asp	Ala	Thr	Glu
			900					905					910		
Ala	Met	Ile	Lys	Gln	Gly	Trp	Thr	Pro	Arg	Arg	Met	Phe	Glu	Glu	Ala
		915					920					925			
Asp	Lys	Phe	Phe	Ile	Ser	Leu	Gly	Leu	Leu	Pro	Val	Pro	Pro	Glu	Phe
	930					935					940				
Trp	Asn	Lys	Ser	Met	Leu	Glu	Lys	Pro	Thr	Asp	Gly	Arg	Glu	Val	Val
945					950					955					960
Cys	His	Ala	Ser	Ala	Trp	Asp	Phe	Tyr	Asn	Gly	Lys	Asp	Phe	Arg	Ile
				965					970					975	



Lys Gln Cys Thr Thr Val Asn Met Glu Asp Leu Val Val Val His His  
980 985 990

Glu Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val  
995 1000 1005

Ala Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp  
1010 1015 1020

Val Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser Ile Asn  
1025 1030 1035 1040

Leu Leu Ser Ser Glu Gly Gly Gly Tyr Glu His Asp Ile Asn Phe Leu  
1045 1050 1055

Met Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu  
1060 1065 1070

Val Asp Glu Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu  
1075 1080 1085

Asn Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu  
1090 1095 1100

Cys Pro Pro Ala Pro Arg Ser Gln Gly Asp Phe Asp Pro Gly Ala Lys  
1105 1110 1115 1120

Phe His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe  
1125 1130 1135

Ile Ile Gln Phe Gln Phe His Glu Ala Leu Cys Lys Ala Ala Gly His  
1140 1145 1150

Thr Gly Pro Leu His Thr Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly  
1155 1160 1165

Lys Arg Leu Ala Asp Ala Met Lys Leu Gly Tyr Ser Lys Pro Trp Pro  
1170 1175 1180

Glu Ala Met Lys Val Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala  
1185 1190 1195 1200

Met Met Asn Tyr Phe Lys Pro Leu Met Asp Trp Leu Leu Thr Glu Asn  
1205 1210 1215

Gly Arg His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Thr Trp Thr Pro  
1220 1225 1230

Asn Ser Ala Arg Ser Glu Gly Ser Leu Pro Asp Ser Gly Arg Val Asn  
1235 1240 1245

Phe Leu Gly Met Asn Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp  
1250 1255 1260

Val Leu Leu Phe Leu Gly Val Ala Leu Leu Leu Ala Ser Leu Gly Leu  
1265 1270 1275 1280

Thr Gln Arg Leu Phe Ser Ile Arg Tyr Gln Ser Leu Arg Gln Pro His  
1285 1290 1295

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His Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser  
 1300 1305 1310

<210> 11

<211> 615

<212> PRT

<213> *Drosophila melanogaster*

<220>

<223> Description of Artificial Sequence: motifs

<400> 11

Met Arg Leu Phe Leu Leu Ala Leu Leu Ala Thr Leu Ala Val Thr Gln  
 1 5 10 15

Ala Leu Val Lys Glu Glu Ile Gln Ala Lys Glu Tyr Leu Glu Asn Leu  
 20 25 30

Asn Lys Glu Leu Ala Lys Arg Thr Asn Val Glu Thr Glu Ala Ala Trp  
 35 40 45

Ala Tyr Gly Ser Asn Ile Thr Asp Glu Asn Glu Lys Lys Lys Asn Glu  
 50 55 60

Ile Ser Ala Glu Leu Ala Lys Phe Met Lys Glu Val Ala Ser Asp Thr  
 65 70 75 80

Thr Lys Phe Gln Trp Arg Ser Tyr Gln Ser Glu Asp Leu Lys Arg Gln  
 85 90 95

Phe Lys Ala Leu Thr Lys Leu Gly Tyr Ala Ala Leu Pro Glu Asp Asp  
 100 105 110

Tyr Ala Glu Leu Leu Asp Thr Leu Ser Ala Met Glu Ser Asn Phe Ala  
 115 120 125

Lys Val Lys Val Cys Asp Tyr Lys Asp Ser Thr Lys Cys Asp Leu Ala  
 130 135 140

Leu Asp Pro Glu Ile Glu Glu Val Ile Ser Lys Ser Arg Asp His Glu  
 145 150 155 160

Glu Leu Ala Tyr Tyr Trp Arg Glu Phe Tyr Asp Lys Ala Gly Thr Ala  
 165 170 175

Val Arg Ser Gln Phe Glu Arg Tyr Val Glu Leu Asn Thr Lys Ala Ala  
 180 185 190

Lys Leu Asn Asn Phe Thr Ser Gly Ala Glu Ala Trp Leu Asp Glu Tyr  
 195 200 205

Glu Asp Asp Thr Phe Glu Gln Gln Leu Glu Asp Ile Phe Ala Asp Ile  
 210 215 220

Arg Pro Leu Tyr Gln Gln Ile His Gly Tyr Val Arg Phe Arg Leu Arg  
 225 230 235 240

Lys His Tyr Gly Asp Ala Val Val Ser Glu Thr Gly Pro Ile Pro Met  
 245 250 255

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His Leu Leu Gly Asn Met Trp Ala Gln Gln Trp Ser Glu Ile Ala Asp  
260 265 270

Ile Val Ser Pro Phe Pro Glu Lys Pro Leu Val Asp Val Ser Ala Glu  
275 280 285

Met Glu Lys Gln Ala Tyr Thr Pro Leu Lys Met Phe Gln Met Gly Asp  
290 295 300

Asp Phe Phe Thr Ser Met Asn Leu Thr Lys Leu Pro Gln Asp Phe Trp  
305 310 315 320

Asp Lys Ser Ile Ile Glu Lys Pro Thr Asp Gly Arg Asp Leu Val Cys  
325 330 335

His Ala Ser Ala Trp Asp Phe Tyr Leu Ile Asp Asp Val Arg Ile Lys  
340 345 350

Gln Cys Thr Arg Val Thr Gln Asp Gln Leu Phe Thr Val His His Glu  
355 360 365

Leu Gly His Ile Gln Tyr Phe Leu Gln Tyr Gln His Gln Pro Phe Val  
370 375 380

Tyr Arg Thr Gly Ala Asn Pro Gly Phe His Glu Ala Val Gly Asp Val  
385 390 395 400

Leu Ser Leu Ser Val Ser Thr Pro Lys His Leu Glu Lys Ile Gly Leu  
405 410 415

Leu Lys Asp Tyr Val Arg Asp Asp Glu Ala Arg Ile Asn Gln Leu Phe  
420 425 430

Leu Thr Ala Leu Asp Lys Ile Val Phe Leu Pro Phe Ala Phe Thr Met  
435 440 445

Asp Lys Tyr Arg Trp Ser Leu Phe Arg Gly Glu Val Asp Lys Ala Asn  
450 455 460

Trp Asn Cys Ala Phe Trp Lys Leu Arg Asp Glu Tyr Ser Gly Ile Glu  
465 470 475 480

Pro Pro Val Val Arg Ser Glu Lys Asp Phe Asp Ala Pro Ala Lys Tyr  
485 490 495

His Ile Ser Ala Asp Val Glu Tyr Leu Arg Tyr Leu Val Ser Phe Ile  
500 505 510

Ile Gln Phe Gln Phe Tyr Lys Ser Ala Cys Ile Lys Ala Gly Gln Tyr  
515 520 525

Asp Pro Asp Asn Val Glu Leu Pro Leu Asp Asn Cys Asp Ile Tyr Gly  
530 535 540

Ser Ala Arg Ala Gly Ala Ala Phe His Asn Met Leu Ser Met Gly Ala  
545 550 555 560

Ser Lys Pro Trp Pro Asp Ala Leu Glu Ala Phe Asn Gly Glu Arg Ile  
565 570 575

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Met Ser Gly Lys Ala Ile Ala Glu Tyr Phe Glu Pro Leu Arg Val Trp  
580 585 590

Leu Glu Ala Glu Asn Ile Lys Asn Asn Val His Ile Gly Trp Thr Thr  
595 600 605

Ser Asn Lys Cys Val Ser Ser  
610 615

<210> 12

<211> 907

<212> PRT

<213> *Caenorhabditis elegans*

<220>

<223> Description of Artificial Sequence: motifs

<400> 12

Met Lys Phe His Ile Leu Leu Leu Leu Leu Val Gly Ala Cys Leu Pro  
1 5 10 15

Val Phe Thr Gln Glu Ile Lys Pro Lys Pro Glu Leu Leu Pro Ala Asp  
20 25 30

Glu Ala Pro Lys Asp Pro Glu Ala Val Phe Ser Glu Gly Glu Pro Phe  
35 40 45

Glu Leu Thr Asp Ala Leu Asp Thr Pro Lys Asn Gly Ser Val Pro Val  
50 55 60

Pro Glu Pro Glu Pro Lys Pro Glu Pro Glu Pro Glu Pro Glu Pro Lys  
65 70 75 80

Pro Glu Pro Glu Pro Ser Pro Thr Pro Glu Pro Glu Pro Ala Ile Lys  
85 90 95

Phe Asp Asn Ile Glu Ser Glu Asp Tyr Gly Asp Val Ala Glu Thr Ala  
100 105 110

Ala Ser Thr Gln Pro Asp Glu Leu Asn Thr Glu Val Ile Glu Gln Leu  
115 120 125

Val Asp Thr Phe Leu Asn Thr Gly Ser Ile Ala Ser Asn Lys Thr Asn  
130 135 140

Lys Gly Pro Val Phe Ala Asn Pro Val Ala Gln Ala Leu Val Asn Ser  
145 150 155 160

Ser Asn Tyr Trp Lys Thr Asp Asn Leu Gln Ala Pro Gly Ser Ile Lys  
165 170 175

Asp Glu Glu Lys Leu Arg Ser Trp Leu Ala Gly Tyr Glu Ala Glu Ala  
180 185 190

Ile Lys Val Leu Arg Glu Val Ala Leu Ser Gly Trp Arg Tyr Phe Asn  
195 200 205

Asp Ala Ser Pro Ser Leu Lys Leu Ala Leu Asp Glu Ala Glu Asn Val  
210 215 220

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Leu Thr Met Phe Val Arg Ser Thr Ser Met Gln Ala Lys Gln Phe Asp  
225 230 235 240

Met Ala Ser Val Thr Asp Glu Lys Val Met Arg Gln Leu Gly Tyr Val  
245 250 255

Ser Phe Glu Gly Met Ser Ala Leu Ala Pro Ser Arg Phe Ala Asp Tyr  
260 265 270

Ser Gln Ala Gln Ala Ala Leu Asn Arg Asp Ser Lys Asp Ser Thr Ile  
275 280 285

Cys Asp Lys Asp Val Pro Pro Pro Cys Ala Leu Gln Lys Ile Asp Met  
290 295 300

Asp Ser Ile Phe Arg Asn Glu Lys Asp Ala Ser Arg Leu Gln His Leu  
305 310 315 320

Trp Val Ser Tyr Val Thr Ala Ile Ala Lys Ser Lys Pro Ser Tyr Asn  
325 330 335

Asn Ile Ile Thr Ile Ser Asn Glu Gly Ala Lys Leu Asn Gly Phe Ala  
340 345 350

Asn Gly Gly Ala Met Trp Arg Ser Ala Phe Asp Met Ser Ser Lys Val  
355 360 365

His Lys Ala Glu Phe Asp Leu Asn Lys Gln Ile Asp Lys Ile Tyr Ser  
370 375 380

Thr Ile Gln Pro Phe Tyr Gln Leu Leu His Ala Tyr Met Arg Arg Gln  
385 390 395 400

Leu Ala Gly Ile Tyr Ser Asn Pro Val Gly Leu Ser Lys Asp Gly Pro  
405 410 415

Ile Pro Ala His Leu Phe Gly Ser Leu Asp Gly Gly Asp Trp Ser Ala  
420 425 430

His Tyr Glu Gln Thr Lys Pro Phe Glu Glu Glu Ser Glu Thr Pro Glu  
435 440 445

Ala Met Leu Ser Ala Phe Asn Thr Gln Asn Tyr Thr Thr Lys Lys Met  
450 455 460

Phe Val Thr Ala Tyr Arg Tyr Phe Lys Ser Ala Gly Phe Pro His Leu  
465 470 475 480

Pro Lys Ser Tyr Trp Thr Ser Ser Ile Phe Ala Arg Val Trp Ser Lys  
485 490 495

Asp Met Ile Cys His Pro Ala Ala Ala Leu Asp Met Arg Ala Pro Asn  
500 505 510

Asp Phe Arg Val Lys Ala Cys Ala Gln Leu Gly Glu Pro Asp Phe Glu  
515 520 525

Gln Ala His Ser Leu Leu Val Gln Thr Tyr Tyr Gln Tyr Leu Tyr Lys  
530 535 540

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Asp Gln Ser Leu Leu Phe Arg Glu Gln Ala Ser Pro Val Ile Thr Asp  
 545 550 555 560  
 Ala Ile Ala Asn Ala Phe Ala His Leu Ser Thr Asn Pro His Tyr Leu  
 565 570 575  
 Tyr Ser Gln Lys Leu Val Pro Ser Glu His Leu Asp Ile Lys Asp Ser  
 580 585 590  
 Val Ile Ile Asn Lys Leu Tyr Lys Glu Ser Leu Glu Ser Phe Thr Lys  
 595 600 605  
 Leu Pro Phe Thr Ile Ala Ala Asp Asn Trp Arg Tyr Glu Leu Phe Asp  
 610 615 620  
 Gly Thr Val Pro Lys Asn Lys Leu Asn Asp Arg Trp Trp Glu Ile Arg  
 625 630 635 640  
 Asn Lys Tyr Glu Gly Val Arg Ser Pro Gln Pro Tyr Asn Thr Ser Asn  
 645 650 655  
 Leu Asp Ala Leu Ile His Asn Ser Val Ser Gln Val His Ser Pro Ala  
 660 665 670  
 Thr Arg Thr Leu Ile Ser Tyr Val Leu Lys Phe Gln Ile Leu Lys Ala  
 675 680 685  
 Leu Cys Gln Arg Glu Leu Phe Trp Leu Ser Glu Gly Cys Ile Leu Ser  
 690 695 700  
 Glu Asp Thr Thr Glu Lys Leu Arg Glu Thr Met Lys Leu Gly Ser Ser  
 705 710 715 720  
 Ile Thr Trp Leu Lys Ala Leu Glu Met Ile Ser Gly Lys Gly Glu Leu  
 725 730 735  
 Asp Ala Gln Pro Leu Leu Glu Tyr Tyr Glu Pro Leu Ile Asn Trp Leu  
 740 745 750  
 Arg Asn Thr Asn Glu Ile Asp Gln Val Val Val Gly Trp Asp Gly Glu  
 755 760 765  
 Gly Thr Pro Phe Thr Val Glu Glu Ile Pro Lys Thr Arg Gln Pro Gly  
 770 775 780  
 Asp Gly Gly Asn Gly Leu Pro Ser Glu Asp Arg Val Ala Phe Pro Gly  
 785 790 795 800  
 Gly Glu Cys Val Asn Gly Gln Glu Cys Leu Leu Asp Ser His Cys Asn  
 805 810 815  
 Gly Thr Ile Cys Val Cys Asn Asp Gly Leu Tyr Thr Leu Glu Ile Gly  
 820 825 830  
 Asn Thr Phe Asn Cys Val Pro Gly Asn Pro Ala Asp Ser Gly Phe Gly  
 835 840 845  
 Asp Gly Lys Gly Gly Leu Val Ile Gly Leu Phe Asn Asn Glu Val Thr  
 850 855 860

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Thr Pro Glu Pro Ser Ala Glu Pro Glu Pro Thr Ala Lys Thr Thr Thr  
865 870 875 880

Lys Met Pro Pro Arg Val Arg Ala Ala Thr Ser Pro Phe Ser Leu Tyr  
885 890 895

Leu Thr Val Leu Leu Ile Ile Tyr Phe Ala Leu  
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<210> 15

<211> 10

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Asp Arg Val Tyr Ile His Pro Phe His Leu  
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<210> 16

<211> 9

<212> PRT

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<223> Description of Artificial Sequence: motifs

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Asp Arg Val Tyr Ile His Pro Phe His  
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<210> 17  
<211> 8  
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<220>  
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<400> 17  
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<210> 18  
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Arg Val Tyr Ile His Pro Phe His Leu  
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Arg Val Tyr Ile His Pro Phe  
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<210> 23

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Lys Ile Asn Glu Thr Glu Asn Ser Ile Asn  
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<400> 24

Ile Ala Arg Arg His Pro Tyr Phe  
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Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly  
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Asp Lys Trp

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Ile Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp  
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Val Gln

0063501.080900

<210> 30  
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atctcacagt caagcttcag ctgc 24

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aggatatctt tatattagca ttctcttcag c 31

<210> 40

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$\langle 210 \rangle$	45
$\langle 211 \rangle$	26

Sensitivity		Specificity		Accuracy		Precision		Recall		F1 Score		ROC AUC		Confusion Matrix	
Model	Value	Model	Value	Model	Value	Model	Value	Model	Value	Model	Value	Model	Value	Model	Value
Model A	0.95	Model A	0.92	Model A	0.93	Model A	0.94	Model A	0.96	Model A	0.95	Model A	0.97	Model A	0.98
Model B	0.91	Model B	0.88	Model B	0.89	Model B	0.90	Model B	0.92	Model B	0.91	Model B	0.93	Model B	0.94
Model C	0.87	Model C	0.85	Model C	0.86	Model C	0.87	Model C	0.89	Model C	0.88	Model C	0.90	Model C	0.91
Model D	0.83	Model D	0.81	Model D	0.82	Model D	0.83	Model D	0.85	Model D	0.84	Model D	0.86	Model D	0.87
Model E	0.79	Model E	0.77	Model E	0.78	Model E	0.79	Model E	0.81	Model E	0.80	Model E	0.82	Model E	0.83
Model F	0.75	Model F	0.73	Model F	0.74	Model F	0.75	Model F	0.77	Model F	0.76	Model F	0.78	Model F	0.79
Model G	0.71	Model G	0.69	Model G	0.70	Model G	0.71	Model G	0.73	Model G	0.72	Model G	0.74	Model G	0.75
Model H	0.67	Model H	0.65	Model H	0.66	Model H	0.67	Model H	0.69	Model H	0.68	Model H	0.70	Model H	0.71
Model I	0.63	Model I	0.61	Model I	0.62	Model I	0.63	Model I	0.65	Model I	0.64	Model I	0.66	Model I	0.67
Model J	0.59	Model J	0.57	Model J	0.58	Model J	0.59	Model J	0.61	Model J	0.60	Model J	0.62	Model J	0.63
Model K	0.55	Model K	0.53	Model K	0.54	Model K	0.55	Model K	0.57	Model K	0.56	Model K	0.58	Model K	0.59
Model L	0.51	Model L	0.49	Model L	0.50	Model L	0.51	Model L	0.53	Model L	0.52	Model L	0.54	Model L	0.55
Model M	0.47	Model M	0.45	Model M	0.46	Model M	0.47	Model M	0.49	Model M	0.48	Model M	0.50	Model M	0.51
Model N	0.43	Model N	0.41	Model N	0.42	Model N	0.43	Model N	0.45	Model N	0.44	Model N	0.46	Model N	0.47
Model O	0.39	Model O	0.37	Model O	0.38	Model O	0.39	Model O	0.41	Model O	0.40	Model O	0.42	Model O	0.43
Model P	0.35	Model P	0.33	Model P	0.34	Model P	0.35	Model P	0.37	Model P	0.36	Model P	0.38	Model P	0.39
Model Q	0.31	Model Q	0.29	Model Q	0.30	Model Q	0.31	Model Q	0.33	Model Q	0.32	Model Q	0.34	Model Q	0.35
Model R	0.27	Model R	0.25	Model R	0.26	Model R	0.27	Model R	0.29	Model R	0.28	Model R	0.30	Model R	0.31
Model S	0.23	Model S	0.21	Model S	0.22	Model S	0.23	Model S	0.25	Model S	0.24	Model S	0.26	Model S	0.27
Model T	0.19	Model T	0.17	Model T	0.18	Model T	0.19	Model T	0.21	Model T	0.20	Model T	0.22	Model T	0.23
Model U	0.15	Model U	0.13	Model U	0.14	Model U	0.15	Model U	0.17	Model U	0.16	Model U	0.18	Model U	0.19
Model V	0.11	Model V	0.09	Model V	0.10	Model V	0.11	Model V	0.13	Model V	0.12	Model V	0.14	Model V	0.15
Model W	0.07	Model W	0.05	Model W	0.06	Model W	0.07	Model W	0.09	Model W	0.08	Model W	0.10	Model W	0.11
Model X	0.03	Model X	0.01	Model X	0.02	Model X	0.03	Model X	0.05	Model X	0.04	Model X	0.06	Model X	0.07
Model Y	0.01	Model Y	0.00	Model Y	0.00	Model Y	0.01	Model Y	0.01	Model Y	0.01	Model Y	0.02	Model Y	0.03
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<210> 46  
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<212> DNA  
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ggtgatatgt ggggtagatt ttgga 25

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ccaacactag gaattactaa cagctt 26

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006080" T055960

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cctgcctctg ttgtctccca tta

24

<210> 51

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: motifs

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gaaaattcca tgctaacgga cccag

25

<210> 52

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: motifs

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tgggatggca gactgctttc tgaa

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<211> 26

<212> DNA

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cggcgcctgg cttatttaatt ttaaga

26

<210> 54

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ctcatacctc ataccttatg tggcaa

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006080 "1.055E960



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tgtacatctg gaaccctca aaag

24

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gaaccacatg gcctctcttc tttc

24

<210> 67

<211> 25

<212> DNA

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<223> Description of Artificial Sequence: motifs

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cagttacccc tgtctcatca tttct

25

<210> 68

<211> 24

<212> DNA

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cagagtatct cctcagactc aaga

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<210> 69

<211> 25

<212> DNA

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ggtcactgac ttaatgaata gcaag

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ggcacacagg aagaacacac aaaat

25

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23

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25

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23

<210> 74  
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23

<210> 75  
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25

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<210> 77  
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24

<210> 78  
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23

<210> 79  
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25

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<212> DNA

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006080" T055E360

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<400> 91  
tgaattgatt attgttgagt gcacag 26

<210> 92  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 92  
cgtctgaatg acaacagcct aga 23

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 93  
cgtctgaatg acgacagcct agag 24

<210> 94  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 94  
agttgaaaac aaggatatatt cattgg 26

<210> 95  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 95  
agttgaaaac aatgatatt cattgg 26

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<210> 96  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 96  
ctagggaaag tcattcagtg gatgtg 26

<210> 97  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: motifs

<400> 97  
ctagggaaag tcgttcagtg gatgtg 26

<210> 98  
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<212> DNA  
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<223> Description of Artificial Sequence: motifs

<400> 98  
ttgaaccagg taagctacta atttt 25

<210> 99  
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<212> DNA  
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ttgaaccagg taggctacta atttt 25

<210> 100  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: motifs

<400> 100  
gttctctaac tgtggagtga atggaaa 27

<210> 101

006080" T055E960



<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 101  
gttctctaac ttagagtg atggaaa

27

<210> 102  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 102  
ggatcacttg taaggacagt gcc

23

<210> 103  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 103  
gatcgattcc aaacatcact gtaggc

26

<210> 104  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 104  
attgaccatt gttggaacac taccg

25

<210> 105  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: motifs

<400> 105  
gtgtgttagc ccctcctggc

20

<210> 106  
<211> 805

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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala  
1 5 10 15  
Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe  
20 25 30  
Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp  
35 40 45  
Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn  
50 55 60  
Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala  
65 70 75 80  
Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln  
85 90 95  
Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys  
100 105 110  
Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser  
115 120 125  
Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu  
130 135 140  
Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu  
145 150 155 160  
Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu  
165 170 175  
Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg  
180 185 190  
Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu  
195 200 205  
Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu  
210 215 220  
Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu  
225 230 235 240  
His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile  
245 250 255  
Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly  
260 265 270  
Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys  
275 280 285  
Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala  
290 295 300

006080" T055960

Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu  
305 310 315 320

Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro  
325 330 335

Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly  
340 345 350

Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp  
355 360 365

Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
370 375 380

Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
385 390 395 400

His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
405 410 415

His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn  
420 425 430

Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
435 440 445

Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe  
450 455 460

Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met  
465 470 475 480

Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr  
485 490 495

Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe  
500 505 510

Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala  
515 520 525

Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile  
530 535 540

Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu  
545 550 555 560

Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala  
565 570 575

Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe  
580 585 590

Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr  
595 600 605

Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu  
610 615 620

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Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met  
625 630 635 640

Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu  
645 650 655

Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val  
660 665 670

Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro  
675 680 685

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile  
690 695 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn  
705 710 715 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln  
725 730 735

Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val  
740 745 750

Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg  
755 760 765

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile  
770 775 780

Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp  
785 790 795 800

Val Gln Thr Ser Phe  
805

<210> 107

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: motifs

<400> 107

Glu Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr Ile Leu  
1 5 10

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